III. AMENDMENT

PLEASE ENTER THE FOLLOWING AMENDMENT WITHOUT PREJUDICE OR DISCLAIMER. Applicants reserve the right to file a divisional or continuation application to the originally filed claims.

1. (Original) A method for determining an organism of interest in a sample from another organism or organisms to be distinguished; said method comprising:

treating the sample, or a portion thereof, with at least one detectable molecular probe wherein the molecular probe or probes are selected such that either:

(i) both the organism of interest and the other organism or organisms react with the molecular probe in a way that produces detectable organisms of interest and a detectable other organism or organisms to be distinguished; or

(ii) only the organism of interest reacts with the molecular probe in a way that produces only detectable organisms of interest; and

contacting the sample, or a portion thereof, with a solid carrier to which has been immobilized a binding partner such that if (i) applies then the binding partner is chosen to be reactive only with the detectable organism of interest but not reactive with the detectable other organism or organisms to be distinguished; but if (ii) applies then the binding partner is chosen to be generally reactive with the detectable organism of interest but also may be reactive with the other organism or organisms to be distinguished; and

determining the presence, absence, position or number of detectable organisms immobilized to the solid carrier and correlating the result with

the presence, absence, or number of the organisms of interest in the sample, or portion thereof.

2. (Original) The method of claim 1, wherein the detectable molecular probe is selected from the group consisting of a nucleic acid and a non-nucleic acid.

3. (Original) The method of claim 2, wherein the non-nucleic acid is a peptide nucleic acid.

4. (Original) The method of claim 1, wherein the detectable molecular probe is not labeled with a detectable moiety.

5. (Original) The method of claim 4, wherein the detectable molecular probe is detected using a detectable antibody that specifically binds to a detectable molecular probe/target sequence complex.

6. (Original) The method of claim 5, wherein the detectable molecular probe is an unlabeled peptide nucleic acid.

7. (Original) The method of claim 1, wherein the detectable molecular probe is labeled with a detectable moiety.

8. (Original) The method of claim 7, wherein the detectable moiety is selected from the group consisting of: a chromophore, a fluorochrome, a spin label, a radioisotope, an enzyme, a hapten and a chemiluminescent compound.

9. (Original) The method of claim 1, wherein the binding partner is an antibody.

10. (Original) The method of claim 1, wherein the binding partner is selected from the group consisting of: a carbohydrate, a lectin, a peptide, a receptor, a charged polymer and a protein.

11. (Original) The method of claim 1, wherein the solid carrier is selected from the group consisting of: a particle, a bead, a microscope slide, a micro titre plate, a membrane and an array.

12. (Original) The method of claim 1, wherein the molecular probe stains all organisms of a domain, kingdom, group, class, genus, species, taxon, subclass, subspecies, serotype or strain without regard to whether or not this represents the organism of interest and wherein the binding partner is specific for the domain, kingdom, group, class, genus, species, taxon, subclass, subspecies, serotype or strain that is the organism of interest.

13. (Original) The method of claim 1, wherein the molecular probe stains only the domain, kingdom, group, class, genus, species, taxon, subclass, subspecies, serotype or strain that is the organism of interest and wherein the binding partner is specific for a particular domain, kingdom, group, class, genus, species, taxon, subclass, subspecies, serotype or strain without regard to whether or not this represents the organism of interest.

14. (Original) The method of claim 1, wherein the molecular probe stains only the domain, kingdom, group, class, genus, species, taxon, subclass, subspecies, serotype or strain that is the organism of interest and wherein the binding partner is specific for only the domain, kingdom, group, class, genus, species, taxon, subclass, subspecies, serotype or strain that is the organism of interest thereby providing an assay that provides certainty at two different levels of molecular discrimination.

15. (Original) The method of claim 1, wherein the sample, or portion thereof, is treated with the detectable molecular probe or probes before being contacted with the solid carrier.

16. (Original) The method of claim 1, wherein the sample, or portion thereof, is contacted with the solid carrier before being treated with the detectable molecular probe or probes.

17. (Original) The method of claim 1, wherein the sample, or portion thereof, is simultaneously contacted with both the solid carrier and treated with the detectable molecular probe or probes.

18. (Original) A method for sorting and determining an organism or organisms of interest in a sample or samples; said method comprising:

treating the sample or samples, or a portion thereof, with one or more detectable or independently detectable molecular probes wherein the one or more molecular probes are selected such that either:

(i) the detectable probe or probes react with the different organisms to be determined in a way that produces different detectable organisms that possess the same stain; or

(ii) the independently detectable probes react with the different organisms to be determined in a way that produces different independently detectable organisms that possess an independently detectable stain; and

contacting the sample or samples, or a portion thereof, with one or more different types of coded beaded supports, wherein each different type of coded beaded support can be independently determined in a suitable particle sorter and wherein to the coded beaded supports have

been immobilized one or more binding partners chosen to select a particular organism or organisms such that the detectable or independently detectable organisms become selectively bound to the coded beaded supports as a result of the occurrence of specific binding partner interactions;

sorting the different types of coded beaded supports in a suitable particle sorter; and

determining the presence, absence, or number of detectable organisms, or each of the independently detectable organisms, immobilized to each different type of coded beaded support and either: (iii) correlating the result with the particular binding partner immobilized to each particle type to thereby determine the presence, absence or number of each of the different organisms of interest in the sample, or portion thereof; or (iv) correlating the result with the code for a sample source from which the sample, or portion thereof, was derived to thereby determine the presence, absence or number of each of the different organisms of interest in each different sample, or portion thereof.

19. (Original) The method of claim 18, wherein the detectable molecular probe is selected from the group consisting of a nucleic acid and a non-nucleic acid.

20. (Original) The method of claim 19, wherein the non-nucleic acid is a peptide nucleic acid.

21. (Original) The method of claim 18, wherein the detectable molecular probe is not labeled with a detectable moiety.

22. (Original) The method of claim 21, wherein the detectable molecular probe is detected using an detectable antibody that specifically binds to a detectable molecular probe/target sequence complex.

23. (Original) The method of claim 22, wherein the detectable molecular probe is an unlabeled peptide nucleic acid.

24. (Original) The method of claim 18, wherein the detectable molecular probe is labeled with a detectable moiety.

25. (Original) The method of claim 24, wherein the detectable moiety is selected from the group consisting of: a chromophore, a fluorochrome, a spin label, a radioisotope, an enzyme, a hapten and a chemiluminescent compound.

26. (Original) The method of claim 18, wherein the independently detectable probes are labeled with independently detectable fluorophores.

27. (Original) The method of claim 18, wherein the particular binding partner is an antibody.

28. (Original) The method of claim 18, wherein the binding partner is selected from the group consisting of: a carbohydrate, a lectin, a peptide, a receptor, a charged polymer and a protein.

29. (Original) The method of claim 18, wherein the sample, or portion thereof, is treated with the detectable or independently detectable molecular probe or probes before being contacted with the solid carrier.

30. (Original) The method of claim 18, wherein the sample, or portion thereof, is contacted with the solid carrier before being treated with the detectable or independently detectable molecular probe or probes.

31. (Original) The method of claim 18, wherein the sample, or portion thereof, is simultaneously contacted with both the solid carrier and treated with the detectable or independently detectable molecular probe or probes.

32. (Original) The method of claim 18, wherein the detectable molecular probe or probes stain all of the different organisms with the same stain and wherein the binding partner is specific for each of the different organisms of interest such that the sorting of the different types of coded beaded supports determines each of the different organisms of interest in the sample, or portion thereof, based solely upon the identity of the different binding partner.

33. (Original) The method of claim 18, wherein the independently detectable molecular probe or probes stain all of the organisms of interest provided that some or all of the different organisms of interest are stained differently and wherein each binding partner associated with each different type of coded beaded support is chosen to select among the same or differently stained organisms such that the sorting of the different types of coded beaded supports when considered in combination with the stain of the organism or organisms bound to each different type of coded beaded support determines each of the different organisms of interest in the sample, or portion thereof.

34. (Original) The method of claim 18, wherein the independently detectable molecular probes stain the organism or organisms of interest differently and

wherein each binding partner associated with each different type of coded beaded support is generic to the chosen assay but each different coded beaded support codes for a different sample such that the determination of the stain or stains on each different coded beaded support specifically determines each of the one or more organisms of interest in the sample, or portion thereof, and each different coded beaded support identifies the source of the sample, or portion thereof.

35. (Original) A method for sorting and determining different organisms of interest in a sample; said method comprising:

treating the sample, or a portion thereof, with one or more detectable or independently detectable molecular probes wherein the one or more molecular probes are selected such that either:

(i) the detectable probe or probes react with the different organisms to be determined in a way that produces different detectable organisms that possess the same stain; or

(ii) the independently detectable probes react with the different organisms to be determined in a way that produces different independently detectable organisms that possess an independently detectable stain; and

contacting the sample, or a portion thereof, with a solid carrier array to which binding partners have been immobilized at unique identifiable locations such that the detectable or independently detectable organisms are selectively bound to the locations on the array as a result of the occurrence of specific binding partner interactions; and

determining the presence, absence or number of the detectable or independently detectable organisms immobilized at the many different locations of the array and correlating the result with the particular binding partner immobilized to each location on the array to thereby determine

the presence, absence or number of the different organisms of interest in the sample.

36. (Original) The method of claim 35, wherein the detectable molecular probe is selected from the group consisting of a nucleic acid and a non-nucleic acid.

37. (Original) The method of claim 36, wherein the non-nucleic acid is a peptide nucleic acid.

38. (Original) The method of claim 35, wherein the detectable molecular probe is not labeled with a detectable moiety.

39. (Original) The method of claim 38, wherein the detectable molecular probe is detected using a detectable antibody that specifically binds to a detectable molecular probe/target sequence complex.

40. (Original) The method of claim 39, wherein the detectable molecular probe is an unlabeled peptide nucleic acid.

41. (Original) The method of claim 35, wherein the detectable molecular probe is labeled with a detectable moiety.

42. (Original) The method of claim 41, wherein the detectable moiety is selected from the group consisting of: a chromophore, a fluorochrome, a spin label, a radioisotope, an enzyme, a hapten and a chemiluminescent compound.

43. (Original) The method of claim 35, wherein the independently detectable probes are labeled with independently detectable fluorophores.

44. (Original) The method of claim 35, wherein the binding partner is an antibody.

45. (Original) The method of claim 35, wherein the binding partner is selected from the group consisting of: a carbohydrate, a lectin, a peptide, a receptor, a charged polymer and a protein.

46. (Original) The method of claim 35, wherein the sample is treated with the detectable or independently detectable molecular probe or probes before being contacted with the solid carrier.

47. (Original) The method of claim 35, wherein the sample is contacted with the solid carrier before being treated with the detectable or independently detectable molecular probe or probes.

48. (Original) The method of claim 35, wherein the sample is simultaneously contacted with both the solid carrier and treating with the detectable or independently detectable molecular probe or probes.

49. (Original) The method of claim 35, wherein the detectable molecular probe or probes stain all of the different organisms with the same stain and wherein the binding partner is specific for each of the different organisms of interest such that the sorting of the organisms on the array resulting from the binding partner interactions occurring at the unique locations is used to thereby determine each of the different organisms of interest in the sample,

or portion thereof, based solely upon the identity of the different binding partners at the unique locations.

50. (Original) The method of claim 35, wherein the independently detectable molecular probe or probes stain all of the organisms of interest provided that some or all of the different organisms of interest are stained differently and wherein each binding partner associated with a unique location on the array is chosen to select among the same or differently stained organisms such that the sorting of the organisms on the array resulting from the binding partner interactions occurring at the unique locations, when considered in combination with the stain of the organism or organisms bound to each unique location, is used to determine each of the different organisms of interest in the sample, or portion thereof.

Claims 51-59 (Canceled)